```
  1 GNTCTAGAANTA GTGGATCCCCCC GGGCTGCAGGAA TTCCGACGGCCC CTGGAAGGGCTC TGGTGGGGCTGA
    CNAGATCTTNAT CACCTAGGGGGG CCCGACGTCCTT AAGGCTGCCGGG GACCTTCCCGAG ACCACCCCGACT

 73 GCGCTCTGCCGC GGGGGCGCGGGC ACAGCAGGAAGC AGGTCCGCGTGG GCGCTGGGGGCA TCAGCTACCGGG
    CGCGAGACGGCG CCCCCGCGCCCG TGTCGTCCTTCG TCCAGGCGCACC CGCGACCCCCGT AGTCGATGGCCC

145 GTGGTCCGGGCT GAAGAGCCAGGC AGCCAAGGCAGC CACCCCGGGGGG TGGGCGACTTTG GGGGAGTTGGTG
    CACCAGGCCCGA CTTCTCGGTCCG TCGGTTCCGTCG GTGGGGCCCCCC ACCCGCTGAAAC CCCCTCAACCAC

217 CCCCGCCCCCCA GGCCTTGGCGGG GTCATGGGGCCC CCCCATTCTGGG CCGGGGGGCGTG CGAGTCGGGGCC
    GGGGCGGGGGGT CCGGAACCGCCC CAGTACCCCGGG GGGGTAAGACCC GGCCCCCCGCAC GCTCAGCCCCGG
  1                                MetGlyPro ProHisSerGly ProGlyGlyVal ArgValGlyAla

289 CTGCTGCTGCTG GGGGTTTTGGGG CTGGTGTCTGGG CTCAGCCTGGAG CCTGTCTACTGG AACTCGGCGAAT
    GACGACGACGAC CCCCAAAACCCC GACCACAGACCC GAGTCGGACCTC GGACAGATGACC TTGAGCCGCTTA
 16 LeuLeuLeuLeu GlyValLeuGly LeuValSerGly LeuSerLeuGlu ProValTyrTrp AsnSerAlaAsn

361 AAGAGGTTCCAG GCAGAGGGTGGT TATGTGCTGTAC CCTCAGATCGGG GACCGGCTAGAC CTGCTCTGCCCC
    TTCTCCAAGGTC CGTCTCCCACCA ATACACGACATG GGAGTCTAGCCC CTGGCCGATCTG GACGAGACGGGG
 40 LysArgPheGln AlaGluGlyGly TyrValLeuTyr ProGlnIleGly AspArgLeuAsp LeuLeuCysPro

433 CGGGCCCGGCCT CCTGGCCCTCAC TCCTCTCCTAAT TATGAGTTCTAC AAGCTGTACCTG GTAGGGGGTGCT
    GCCCGGGCCGGA GGACCGGGAGTG AGGAGAGGATTA ATACTCAAGATG TTCGACATGGAC CATCCCCCACGA
 64 ArgAlaArgPro ProGlyProHis SerSerProAsn TyrGluPheTyr LysLeuTyrLeu ValGlyGlyAla

505 CAGGGCCGGCGC TGTGAGGCACCC CCTGCCCCAAAC CTCCTTCTCACT TGTGATCGCCCA GACCTGGATCTC
    GTCCCGGCCGCG ACACTCCGTGGG GGACGGGGTTTG GAGGAAGAGTGA ACACTAGCGGGT CTGGACCTAGAG
 88 GlnGlyArgArg CysGluAlaPro ProAlaProAsn LeuLeuLeuThr CysAspArgPro AspLeuAspLeu

577 CGCTTCACCATC AAGTTCCAGGAG TATAGCCCTAAT CTCTGGGGCCAC GAGTTCCGCTCG CACCACGATTAC
    GCGAAGTGGTAG TTCAAGGTCCTC ATATCGGGATTA GAGACCCCGGTG CTCAAGGCGAGC GTGGTGCTAATG
112 ArgPheThrIle LysPheGlnGlu TyrSerProAsn LeuTrpGlyHis GluPheArgSer HisHisAspTyr
```

FIG._1A

```
649  TACATCATTGCC ACATCGGATGGG ACCCGGGAGGGC CTGGAGAGCCTG CAGGGAGGTGTG TGCCTAACCAGA
     ATGTAGTAACGG TGTAGCCTACCC TGGGCCCTCCCG GACCTCTCGGAC GTCCCTCCACAC ACGGATTGGTCT
136  TyrIleIleAla ThrSerAspGly ThrArgGluGly LeuGluSerLeu GlnGlyGlyVal CysLeuThrArg

721  GGCATGAAGGTG CTTCTCCGAGTG GGACAAAGTCCC CGAGGAGGGGCT GTCCCCCGAAAA CCTGTGTCTGAA
     CCGTACTTCCAC GAAGAGGCTCAC CCTGTTTCAGGG GCTCCTCCCCGA CAGGGGGCTTTT GGACACAGACTT
160  GlyMetLysVal LeuLeuArgVal GlyGlnSerPro ArgGlyGlyAla ValProArgLys ProValSerGlu

793  ATGCCCATGGAA AGAGACCGAGGG GCAGCCCACAGC CTGGAGCCTGGG AAGGAGAACCTG CCAGGTGACCCC
     TACGGGTACCTT TCTCTGGCTCCC CGTCGGGTGTCG GACCTCGGACCC TTCCTCTTGGAC GGTCCACTGGGG
184  MetProMetGlu ArgAspArgGly AlaAlaHisSer LeuGluProGly LysGluAsnLeu ProGlyAspPro

865  ACCAGCAATGCA ACCTCCCGGGGT GCTGAAGGCCCC CTGCCCCCTCCC AGCATGCCTGCA GTGGCTGGGGCA
     TGGTCGTTACGT TGGAGGGCCCCA CGACTTCCGGGG GACGGGGGAGGG TCGTACGGACGT CACCGACCCCGT
208  ThrSerAsnAla ThrSerArgGly AlaGluGlyPro LeuProProPro SerMetProAla ValAlaGlyAla

937  GCAGGGGGGCTG GCGCTGCTCTTG CTGGGCGTGGCA GGGGCTGGGGGT GCCATGTGTTGG CGGAGACGGCGG
     CGTCCCCCCGAC CGCGACGAGAAC GACCCGCACCGT CCCCGACCCCCA CGGTACACAACC GCCTCTGCCGCC
232  AlaGlyGlyLeu AlaLeuLeuLeu LeuGlyValAla GlyAlaGlyGly AlaMetCysTrp ArgArgArgArg

1009 GCCAAGCCTTCG GAGAGTCGCCAC CCTGGTCCTGGC TCCTTCGGGAGG GGAGGGTCTCTG GGCCTGGGGGGT
     CGGTTCGGAAGC CTCTCAGCGGTG GGACCAGGACCG AGGAAGCCCTCC CCTCCCAGAGAC CCGGACCCCCCA
256  AlaLysProSer GluSerArgHis ProGlyProGly SerPheGlyArg GlyGlySerLeu GlyLeuGlyGly

1081 GGAGGTGGGATG GGACCTCGGGAG GCTGAGCCTGGG GAGCTAGGGATA GCTCTGCGGGGT GGCGGGGCTGCA
     CCTCCACCCTAC CCTGGAGCCCTC CGACTCGGACCC CTCGATCCCTAT CGAGACGCCCCA CCGCCCCGACGT
280  GlyGlyGlyMet GlyProArgGlu AlaGluProGly GluLeuGlyIle AlaLeuArgGly GlyGlyAlaAla

1153 GATCCCCCCTTC TGCCCCCACTAT GAGAAGGTGAGT GGTGACTATGGG CATCCTGTGTAT ATCGTGCAGGAT
     CTAGGGGGGAAG ACGGGGGTGATA CTCTTCCACTCA CCACTGATACCC GTAGGACACATA TAGCACGTCCTA
304  AspProProPhe CysProHisTyr GluLysValSer GlyAspTyrGly HisProValTyr IleValGlnAsp

1225 GGGCCCCCCCAG AGCCCTCCAAAC ATCTACTACACA TCGATTTCTGTG TTGGAGTGGCCC ATATTGCATACG
     CCCGGGGGGGTC TCGGGAGGTTTG TAGATGATGTGT AGCTAAAGACAC AACCTCACCGGG TATAACGTATGC
328  GlyProProGln SerProProAsn IleTyrTyrThr SerIleSerVal LeuGluTrpPro IleLeuHisThr
```

FIG._1B

```
1297  ATACAACTGTTT TTCATGCGATCC AAGTGCTCCCGT GTCACTACATTC TTATTTCCTGTG CAAGTTATTACG
      TATGTTGACAAA AAGTACGCTAGG TTCACGAGGGCA CAGTGATGTAAG AATAAAGGACAC GTTCAATAATGC
 352  IleGlnLeuPhe PheMetArgSer LysCysSerArg ValThrThrPhe LeuPheProVal GlnValIleThr

1369  ACATCGACTTGC CGGATGACTTCA TTTAGCTTTACC ACCCTGAACCCA TCCATGCAGGCC TGCAGAGCACAG
      TGTAGCTGAACG GCCTACTGAAGT AAATCGAAATGG TGGGACTTGGGT AGGTACGTCCGG ACGTCTCGTGTC
 376  ThrSerThrCys ArgMetThrSer PheSerPheThr ThrLeuAsnPro SerMetGlnAla CysArgAlaGln

1441  ATGGGGGAATTC CGAATCAGATGG TGTTTCTGGGGG GACAGGATCCTG GGTACGGCTCTG TTTGTGCTTGTG
      TACCCCCTTAAG GCTTAGTCTACC ACAAAGACCCCC CTGTCCTAGGAC CCATGCCGAGAC AAACACGAACAC
 400  MetGlyGluPhe ArgIleArgTrp CysPheTrpGly AspArgIleLeu GlyThrAlaLeu PheValLeuVal

1513  CTTATTCTTCTT CTTGGGAGGCTG AATATGCATCAG ACGACACTGCTC CGGCAACGGGCC AGTGTGGAGGCG
      GAATAAGAAGAA GAACCCTCCGAC TTATACGTAGTC TGCTGTGACGAG GCCGTTGCCCGG TCACACCTCCGC
 424  LeuIleLeuLeu LeuGlyArgLeu AsnMetHisGln ThrThrLeuLeu ArgGlnArgAla SerValGluAla

1585  GAAGCCGGCCAG CATGGTCCCCTG TGATAGGATTGA AAGAGCTACTGA GAATAGGGGGCT TCTCAATGAGAG
      CTTCGGCCGGTC GTACCAGGGGAC ACTATCCTAACT TTCTCGATGACT CTTATCCCCCGA AGAGTTACTCTC
 448  GluAlaGlyGln HisGlyProLeu

1657  AGCGGAGGCTGC TGTTATCATGGG AACCAGGCAGAT CAATCATCCCTG GCAGGTCAGGCA GGAAGTTACTTA
      TCGCCTCCGACG ACAATAGTACCC TTGGTCCGTCTA GTTAGTAGGGAC CGTCCAGTCCGT CCTTCAATGAAT

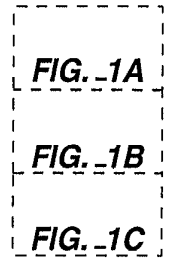
1729  GCTTCTCCTTCA CCTTCTTCCCAC AGAATTTATTAT AGGCTTGTTCCA AGTTGTAGTGTG TGATCAGATTCG
      CGAAGAGGAAGT GGAAGAAGGGTG TCTTAAATAATA TCCGAACAAGGT TCAACATCACAC ACTAGTCTAAGC

1801  TGCTGCCTGTCA GCTCTGTGCTAC CTGGCAGTTCCC CTCATGGAATTC GATATCAAGCTT ATCGATACCGTC
      ACGACGGACAGT CGAGACACGATG GACCGTCAAGGG GAGTACCTTAAG CTATAGTTCGAA TAGCTATGGCAG

1873  GACCT
      CTGGA
```

FIG._1C

FIG._1



```
  1  GNTCTAGAANTA GTGGATCCCCCC GGGCTGCAGGAA TTCCGACGGCCC CTGGAAGGGCTC TGGTGGGGCTGA
     CNAGATCTTNAT CACCTAGGGGGG CCCGACGTCCTT AAGGCTGCCGGG GACCTTCCCGAG ACCACCCCGACT

 73  GCGCTCTGCCGC GGGGGCGCGGGC ACAGCAGGAAGC AGGTCCGCGTGG GCGCTGGGGGCA TCAGCTACCGGG
     CGCGAGACGGCG CCCCCGCGCCCG TGTCGTCCTTCG TCCAGGCGCACC CGCGACCCCCGT AGTCGATGGCCC

145  GTGGTCCGGGCT GAAGAGCCAGGC AGCCAAGGCAGC CACCCCGGGGGG TGGGCGACTTTG GGGGAGTTGGTG
     CACCAGGCCCGA CTTCTCGGTCCG TCGGTTCCGTCG GTGGGGCCCCCC ACCCGCTGAAAC CCCCTCAACCAC

217  CCCCGCCCCCCA GGCCTTGGCGGG GTCATGGGGCCC CCCCATTCTGGG CCGGGGGGCGTG CGAGTCGGGGCC
     GGGGCGGGGGGT CCGGAACCGCCC CAGTACCCCGGG GGGGTAAGACCC GGCCCCCCGCAC GCTCAGCCCCGG
   1                                MetGlyPro ProHisSerGly ProGlyGlyVal ArgValGlyAla

289  CTGCTGCTGCTG GGGGTTTTGGGG CTGGTGTCTGGG CTCAGCCTGGAG CCTGTCTACTGG AACTCGGCGAAT
     GACGACGACGAC CCCCAAAACCCC GACCACAGACCC GAGTCGGACCTC GGACAGATGACC TTGAGCCGCTTA
  16 LeuLeuLeuLeu GlyValLeuGly LeuValSerGly LeuSerLeuGlu ProValTyrTrp AsnSerAlaAsn

361  AAGAGGTTCCAG GCAGAGGGTGGT TATGTGCTGTAC CCTCAGATCGGG GACCGGCTAGAC CTGCTCTGCCCC
     TTCTCCAAGGTC CGTCTCCCACCA ATACACGACATG GGAGTCTAGCCC CTGGCCGATCTG GACGAGACGGGG
  40 LysArgPheGln AlaGluGlyGly TyrValLeuTyr ProGlnIleGly AspArgLeuAsp LeuLeuCysPro

433  CGGGCCCGGCCT CCTGGCCCTCAC TCCTCTCCTAAT TATGAGTTCTAC AAGCTGTACCTG GTAGGGGGTGCT
     GCCCGGGCCGGA GGACCGGGAGTG AGGAGAGGATTA ATACTCAAGATG TTCGACATGGAC CATCCCCCACGA
  64 ArgAlaArgPro ProGlyProHis SerSerProAsn TyrGluPheTyr LysLeuTyrLeu ValGlyGlyAla

505  CAGGGCCGGCGC TGTGAGGCACCC CCTGCCCCAAAC CTCCTTCTCACT TGTGATCGCCCA GACCTGGATCTC
     GTCCCGGCCGCG ACACTCCGTGGG GGACGGGGTTTG GAGGAAGAGTGA ACACTAGCGGGT CTGGACCTAGAG
  88 GlnGlyArgArg CysGluAlaPro ProAlaProAsn LeuLeuLeuThr CysAspArgPro AspLeuAspLeu

577  CGCTTCACCATC AAGTTCCAGGAG TATAGCCCTAAT CTCTGGGGCCAC GAGTTCCGCTCG CACCACGATTAC
     GCGAAGTGGTAG TTCAAGGTCCTC ATATCGGGATTA GAGACCCCGGTG CTCAAGGCGAGC GTGGTGCTAATG
 112 ArgPheThrIle LysPheGlnGlu TyrSerProAsn LeuTrpGlyHis GluPheArgSer HisHisAspTyr
```

FIG._2A

```
649  TACATCATTGCC ACATCGGATGGG ACCCGGGAGGGC CTGGAGAGCCTG CAGGGAGGTGTG TGCCTAACCAGA
     ATGTAGTAACGG TGTAGCCTACCC TGGGCCCTCCCG GACCTCTCGGAC GTCCCTCCACAC ACGGATTGGTCT
136  TyrIleIleAla ThrSerAspGly ThrArgGluGly LeuGluSerLeu GlnGlyGlyVal CysLeuThrArg

721  GGCATGAAGGTG CTTCTCCGAGTG GGACAAAGTCCC CGAGGAGGGGCT GTCCCCCGAAAA CCTGTGTCTGAA
     CCGTACTTCCAC GAAGAGGCTCAC CCTGTTTCAGGG GCTCCTCCCCGA CAGGGGGCTTTT GGACACAGACTT
160  GlyMetLysVal LeuLeuArgVal GlyGlnSerPro ArgGlyGlyAla ValProArgLys ProValSerGlu

793  ATGCCCATGGAA AGAGACCGAGGG GCAGCCCACAGC CTGGAGCCTGGG AAGGAGAACCTG CCAGGTGACCCC
     TACGGGTACCTT TCTCTGGCTCCC CGTCGGGTGTCG GACCTCGGACCC TTCCTCTTGGAC GGTCCACTGGGG
184  MetProMetGlu ArgAspArgGly AlaAlaHisSer LeuGluProGly LysGluAsnLeu ProGlyAspPro

865  ACCAGCAATGCA ACCTCCCGGGGT GCTGAAGGCCCC CTGCCCCCTCCC AGCATGCCTGCA GTGGCTGGGGCA
     TGGTCGTTACGT TGGAGGGCCCCA CGACTTCCGGGG GACGGGGGAGGG TCGTACGGACGT CACCGACCCCGT
208  ThrSerAsnAla ThrSerArgGly AlaGluGlyPro LeuProProPro SerMetProAla ValAlaGlyAla

937  GCAGGGGGGCTG GCGCTGCTCTTG CTGGGCGTGGCA GGGGCTGGGGGT GCCATGTGTTGG CGGAGACGGCGG
     CGTCCCCCCGAC CGCGACGAGAAC GACCCGCACCGT CCCCGACCCCCA CGGTACACAACC GCCTCTGCCGCC
232  AlaGlyGlyLeu AlaLeuLeuLeu LeuGlyValAla GlyAlaGlyGly AlaMetCysTrp ArgArgArgArg

1009 GCCAAGCCTTCG GAGAGTCGCCAC CCTGGTCCTGGC TCCTTCGGGAGG GGAGGGTCTCTG GGCCTGGGGGGT
     CGGTTCGGAAGC CTCTCAGCGGTG GGACCAGGACCG AGGAAGCCCTCC CCTCCCAGAGAC CCGGACCCCCCA
256  AlaLysProSer GluSerArgHis ProGlyProGly SerPheGlyArg GlyGlySerLeu GlyLeuGlyGly

1081 GGAGGTGGGATG GGACCTCGGGAG GCTGAGCCTGGG GAGCTAGGGATA GCTCTGCGGGGT GGCGGGGCTGCA
     CCTCCACCCTAC CCTGGAGCCCTC CGACTCGGACCC CTCGATCCCTAT CGAGACGCCCCA CCGCCCCGACGT
280  GlyGlyGlyMet GlyProArgGlu AlaGluProGly GluLeuGlyIle AlaLeuArgGly GlyGlyAlaAla

1153 GATCCCCCCTTC TGCCCCCACTAT GAGAAGGTGAGT GGTGACTATGGG CATCCTGTGTAT ATCGTGCAGGAT
     CTAGGGGGGAAG ACGGGGGTGATA CTCTTCCACTCA CCACTGATACCC GTAGGACACATA TAGCACGTCCTA
304  AspProProPhe CysProHisTyr GluLysValSer GlyAspTyrGly HisProValTyr IleValGlnAsp

1225 GGGCCCCCCCAG AGCCCTCCAAAC ATCTACTACAAG GTATGAGGGCTC CTCTCACGTGGC TATCCTGAATCC
     CCCGGGGGGGTC TCGGGAGGTTTG TAGATGATGTTC CATACTCCCGAG GAGAGTGCACCG ATAGGACTTAGG
328  GlyProProGln SerProProAsn IleTyrTyrLys ValOP*
```

FIG._2B

```
1297  AGCCCTTCTTGG GGTGCTCCTCCA GTTTAATTCCTG GTTTGAGGGACA CCTCTAACATCT CGGCCCCCTGTG
      TCGGGAAGAACC CCACGAGGAGGT CAAATTAAGGAC CAAACTCCCTGT GGAGATTGTAGA GCCGGGGGACAC

1369  CCCCCCCAGCCC CTTCACTCCTCC CGGCTGCTGTCC TCGTCTCCACTT TTAGGATTCCTT AGGATTCCCACT
      GGGGGGGTCGGG GAAGTGAGGAGG GCCGACGACAGG AGCAGAGGTGAA AATCCTAAGGAA TCCTAAGGGTGA

1441  GCCCCACTTCCT GCCCTCCCGTTT GGCCATGGGTGC CCCCCTCTGTCT CAGTGTCCCTGG ATCCTTTTTCCT
      CGGGGTGAAGGA CGGGAGGGCAAA CCGGTACCCACG GGGGGAGACAGA GTCACAGGGACC TAGGAAAAAGGA

1513  TGGGGAGGGGCA CAGGCTCAGCCT CCTCTCTGACCA TGACCCAGGCAT CCTTGTCCCCCT CACCCACCCAGA
      ACCCCTCCCCGT GTCCGAGTCGGA GGAGAGACTGGT ACTGGGTCCGTA GGAACAGGGGGA GTGGGTGGGTCT

1585  GCTAGGGGCGGG AACAGCCCACCT TTTGGTTGGCAC CGCCTTCTTTCT GCCTCTCACTGG TTTTCTCTTCTC
      CGATCCCCGCCC TTGTCGGGTGGA AAACCAACCGTG GCGGAAGAAAGA CGGAGAGTGACC AAAAGAGAAGAG

1657  TATCTCTTATTC TTTCCCTCTCTT CCGTCTCTAGGT CTGTTCTTCTTC CCTAGCATCCTC CTCCCCACATCT
      ATAGAGAATAAG AAAGGGAGAGAA GGCAGAGATCCA GACAAGAAGAAG GGATCGTAGGAG GAGGGGTGTAGA

1729  CCTTTCACCCTC TTGGCTTCTTAT CCTGTGCCTCTC CCATCTCCTGGG TGGGGGCATCAA AGCATTTCTCCC
      GGAAAGTGGGAG AACCGAAGAATA GGACACGGAGAG GGTAGAGGACCC ACCCCCGTAGTT TCGTAAAGAGGG

1801  CTTAGCTTTCAG CCCCCCTTCTGA CCTCTCATACCA ACCACTCCCCTC AGTCTGCCAAAA ATGGGGGCCTTA
      GAATCGAAAGTC GGGGGGAAGACT GGAGAGTATGGT TGGTGAGGGGAG TCAGACGGTTTT TACCCCCGGAAT

1873  TGGGGAAGGCTC TGACACTCCACC CCAGCTCAGGCC ATGGGCACCAGG GCTCCATTCTCT GGCCTGGCCCAG
      ACCCCTTCCGAG ACTGTGAGGTGG GGTCGAGTCCGG TACCCGTCGTCC CGAGGTAAGAGA CCGGACCGGGTC

1945  GCCTCTACATAC TTACTCCAGCCA TTTGGGGTGGTT GGGTCATGACAG CTACCATGAGAA GAAGTGTCCCGT
      CGGAGATGTATG AATGAGGTCGGT AAACCCCACCAA CCCAGTACTGTC GATGGTACTCTT CTTCACAGGGCA

2017  TTTGTCCAGTGG CCAATAGCAAGA TATGAACCGGTC GGGACATGTATG GACTTGGTCTGA TGCTGAATGGGC
      AAACAGGTCACC GGTTATCGTTCT ATACTTGGCCAG CCCTGTACATAC CTGAACCAGACT ACGACTTACCCG
```

FIG._2C

```
2089  CACTTGGGACCG GAAGTGACTTGC TCCAGACAAGAG GTGACCAGGCCC GGACAGAAATGG CCTGGGAAGTAG
      GTGAACCCTGGC CTTCACTGAACG AGGTCTGTTCTC CACTGGTCCGGG CCTGTCTTTACC GGACCCTTCATC

2161  CAGAAGCAGTGC AGCAGGAACTGG AAGTGCCTTCAT CCAGGACAGGAA GTAGCACTTCTG AAACAGGAAGTG
      GTCTTCGTCACG TCGTCCTTGACC TTCACGGAAGTA GGTCCTGTCCTT CATCGTGAAGAC TTTGTCCTTCAC

2233  GTCTGGCTGGAA CTCCAAGTGGCT TAGTCTGGGGGA TCAGGAGGTGGG AGGTGGATGGTT CTTATTCTGTGG
      CAGACCGACCTT GAGGTTCACCGA ATCAGACCCCCT AGTCCTCCACCC TCCACCTACCAA GAATAAGACACC

2305  AGAAGAAGGGCG GGAAGAACTTCC TTTCAGGAGGAA GCTGGAACTTAC TGACTGTAAGAG GTTAGAGGTGGA
      TCTTCTTCCCGC CCTTCTTGAAGG AAAGTCCTCCTT CGACCTTGAATG ACTGACATTCTC CAATCTCCACCT

2377  CCGA
      GGCT
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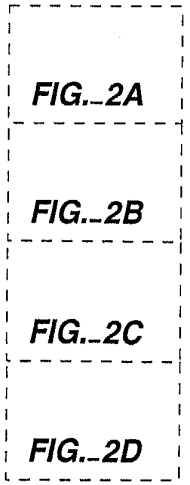
FIG._2D

FIG._2



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AL-2b.L     1 G N T C T A G A A N T A G T G G A T C C C C C C G G G C T G C A G G A A T T C C G A C G G C C C C T
AL-2b.L    51 G G A A G G G C T C T G G T G G G G C T G A G C G C T C T G C C G C G G G G G C G C G G G C A C A G
AL-2b.L   101 C A G G A A G C A G G T C C G C G T G G G C G C T G G G G G C A T C A G C T A C C G G G G T G G T C
AL-2b.L   151 C G G G C T G A A G A G C C A G G C A G C C A A G G C A G C C A C C C C G G G G G G T G G G C G A C
AL-2b.L   201 T T T G G G G G A G T T G G T G C C C C G C C C C C C A G G C C T T G G C G G G G T C A T G G G G C
AL-2b.L   251 C C C C C C A T T C T G G G C C G G G G G G C G T G C G A G T C G G G G C C C T G C T G C T G C T G
AL-2b.L   301 G G G G T T T T G G G G C T G G T G T C T G G G C T C A G C C T G G A G C C T G T C T A C T G G A A
AL-2b.L   351 C T C G G C G A A T A A G A G G T T C C A G G C A G A G G G T G G T T A T G T G C T G T A C C C T C
AL-2b.L   401 A G A T C G G G G A C C G G C T A G A C C T G C T C T G C C C C C G G G C C C G G C C T C C T G G C
AL-2b.L   451 C C T C A C T C C T C T C C T A A T T A T G A G T T C T A C A A G C T G T A C C T G G T A G G G G G
AL-2b.L   501 T G C T C A G G G C C G G C G C T G T G A G G C A C C C C C T G C C C C A A A C C T C C T T C T C A
H10006      1 - - - - - - - - - G C C G A C G C T G T G A G G C A C C C C C T G C C C C A A A C C T C C T T C T C A
AL-2b.L   551 C T T G T G A T C G C C C A G A C C T G G A T C T C C G C T T C A C C A T C A A G T T C C A G G A G
H10006     43 C T T G T G A T C G C C C A G A C C T G G A T C T C C G C T T C A C C A T C A A G T T C C A G G A G
AL-2b.L   601 T A T A G C C C T A A T C T C T G G G G C C A C G A G T T C C G C T C G C A C C A C G A T T A C T A
H10006     93 T A T A G C C C T A A T C T C T G G G G C C A C G A G T T C C G C T C G C A C C A C G A T T A C T A
AL-2b.L   651 C A T C A T T G C C A C A T C G G A T G G G A C C C G G G A G G G C C T G G A G A G C C T G C A G G
H10006    143 C A T C A T T G C C A C A T C G G A T G G G A C C C G G G A G G C C T G G A G A G C C T G C A G G
AL-2b.L   701 G A G G T G T G T G C C T A A C C A G A G G C A T G A A G G T G C T T C T C C G A G T G G G A C A A
H10006    193 G A A G T G T G T G C C T A A C C A G A G G C A T G A A G G T G C T T C T C C G A G T N G G A C A A
```

FIG._3A

```
AL-2b.L   751 AGTCCCCGAGGAGGGGCTGTCCCCCGAAAACCTGTGTCTGAAATGCCCAT
H10006    243 AGT-CCCGAGGAGGGGCTGTCCCCCGAAAACCTGTGTCTGAAATGCCCAT

AL-2b.L   801 GGAAAGAGACCGAGGGGCAGCCCACAGCCT-GGAGCCT-GGGAAGGAGAA
H10006    292 GGAAAGAGACCGAGGGGCAGCCCACAGCCTGGAGCCTGGGAAGGAGAA

AL-2b.L   849 CCTGCCAGGTGACCCCACCAGCAATGCAACCTCCCGGGGT--GCTGAAGG
H10006    342 CCTGCCAGGTGACCCCACCAGCAATNCAACCTTCCGGGGTTGCTTGAAGG

AL-2b.L   897 CCCCCT--GCCCCCTCCCAGCA-TGCCTGCAGT--GGCTGGGGCAGCAGG
H10006    392 GCCCCTTGACCCTTTCCCAGCATTGCNTGCANTTGGTTNGGGGCAGCANG

AL-2b.L   942 GGGGC----TGGCGCTGCTCTTGCTGGGCGTGGCAGGGGCTGGGGGGTGCC
H10006    442 GGGGNGTTTTGGC

AL-2b.L   988 ATGTGTTGGCGGAGACGGCGGGCCAAGCCTTCGGAGAGTCGCCACCCTGG

AL-2b.L  1038 TCCTGGCTCCTTCGGGAGGGGAGGGTCTCTGGGCCTGGGGGGGTGGAGGTG

AL-2b.L  1088 GGATGGGACCTCGGGAGGCTGAGCCTGGGGAGCTAGGGATAGCTCTGCGG

AL-2b.L  1138 GGTGGCGGGGCTGCAGATCCCCCCTTCTGCCCCCACTATGAGAAGGTGAG

AL-2b.L  1188 TGGTGACTATGGGCATCCTGTGTATATCGTGCAGGATGGGCCCCCCCAGA

AL-2b.L  1238 GCCCTCCAAACATCTACTACACATCGATTTCTGTGTTGGAGTGGCCCATA

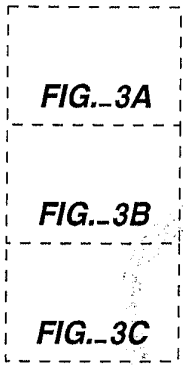
AL-2b.L  1288 TTGCATACGATACAACTGTTTTTCATGCGATCCAAGTGCTCCCGTGTCAC
```

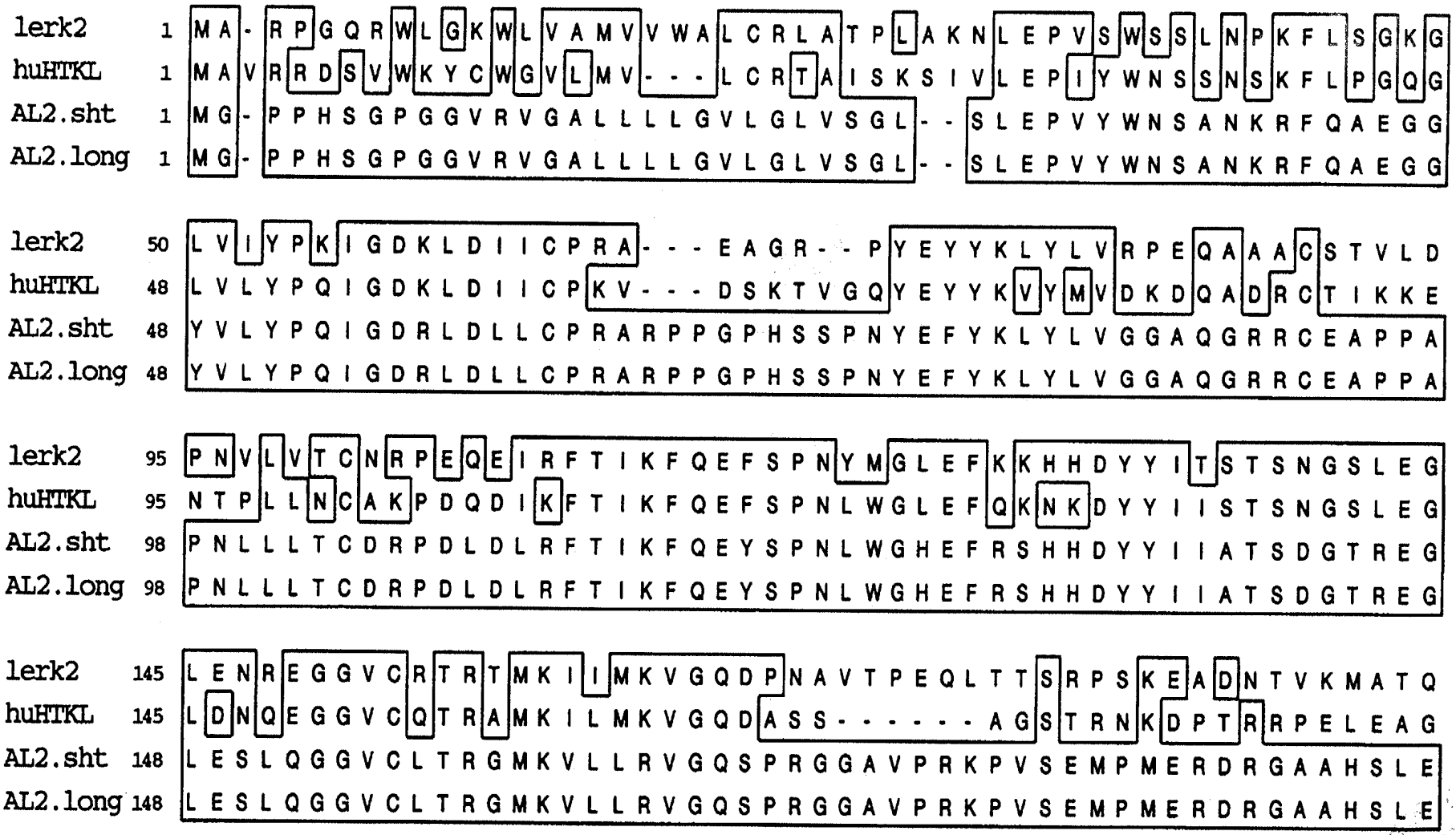

FIG._3B

```
AL-2b.L 1338 T A C A T T C T T A T T T C C T G T G C A A G T T A T T A C G A C A T C G A C T T G C C G G A T G A
AL-2b.L 1388 C T T C A T T T A G C T T T A C G A C C C T G A A C C C A T C C A T G C A G G C C T G C A G A G C A
AL-2b.L 1438 C A G A T G G G G G A A T T C C G A A T C A G A T G G T G T T T C T G G G G G G A C A G G A T C C T
AL-2b.L 1488 G G G T A C G G C T C T G T T T G T G C T T G T G C T T A T T C T T C T T C T T G G G A G G C T G A
AL-2b.L 1538 A T A T G C A T C A G A C G A C A G T G C T C C G G C A A C G G G C C A G T G T G G A G G C G G A A
AL-2b.L 1588 G C C G G C C A G C A T G G T C C G C T G T G A T A G G A T T G A A A G A G C T A C T G A G A A T A
AL-2b.L 1638 G G G G G C T T C T C A A T G A G A G A G C G G A G G C T G C T G T T A T C A T G G G A A C C A G G
AL-2b.L 1688 C A G A T C A A T C A T C C C T G G C A G G T C A G G C A G G A A G T T A C T T A G C T T C T C C T
AL-2b.L 1738 T C A C C T T C T T C C C A C A G A A T T T A T T A T A G G C T T G T T C C A A G T T G T A G T G T
AL-2b.L 1788 G T G A T C A G A T T C G T G C T G C C T G T C A G C T C T G T G C T A C C T G G C A G T T C C C C
AL-2b.L 1838 T C A T G G A A T T C G A T A T C A A G C T T A T C G A T A C C G T C G A C C T
```

FIG._3C

FIG._3

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huHTKL 1 MAVRRDSVWKYCWGVLMV---LCRTAISKSIVLEPIYWNSSNSKFLPGQG
AL2.sht 1 MG-PPHSGPGGVRVGALLLLGVLGLVSGL--SLEPVYWNSANKRFQAEGG
AL2.long 1 MG-PPHSGPGGVRVGALLLLGVLGLVSGL--SLEPVYWNSANKRFQAEGG
lerk2 50 LVIYPKIGDKLDIICPRA---EAGR--PYEYYKLYLVRPEQAAACSTVLD
huHTKL 48 LVLYPQIGDKLDIICPKV---DSKTVGQYEYYKVYMVDKDQADRCTIKKE
AL2.sht 48 YVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPA
AL2.long 48 YVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPA
lerk2 95 PNVLVTCNRPEQEIRFTIKFQEFSPNYMGLEFKKHHDYYITSTSNGSLEG
huHTKL 95 NTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNKDYYIISTSNGSLEG
AL2.sht 98 PNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREG
AL2.long 98 PNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREG
lerk2 145 LENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTTSRPSKEADNTVKMATQ
huHTKL 145 LDNQEGGVCQTRAMKILMKVGQDASS------AGSTRNKDPTRRPELEAG
AL2.sht 148 LESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLE
AL2.long 148 LESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLE

FIG._4A

```
lerk2      195 A P G S R G S L G D S D G K H E T V N Q E E K S G P G A S G G S S G D P D G F F N S K V A L F A A V
huHTKL     189 T N G - R S S T T S P F V K P N P G S S T D G N S A G H S G - - - - - - N N I L G S E V A L F A G I
AL2.sht    198 - P G K E N L P G D P T S N A T S R G A E G P L P P P S M P A V A G A A G G L - - - A L L L L G V A
AL2.long   198 - P G K E N L P G D P T S N A T S R G A E G P L P P P S M P A V A G A A G G L - - - A L L L L G V A

lerk2      245 G A G C V I F L L I I I F L T V L L L K L R K R H R K H T Q - Q R A A A L S L S T L A S P K G G S G
huHTKL     232 A S G C I I F I V I I I T L V V L L L K Y R R R H R K H S P - Q H T T T L S L S T L A T P K R S G N
AL2.sht    244 G A G G A - - - - - M C W R R R R A K P S E S R H P G P G S F G R G G S L G L G G - - - - G G G M G
AL2.long   244 G A G G A - - - - - M C W R R R R A K P S E S R H P G P G S F G R G G S L G L G G - - - - G G G M G

lerk2      294 T A G T E P S D I I I P L R - - - T T E N N Y C P H Y E K V S G D Y G H P V Y I V Q E M P P Q S P A
huHTKL     281 N N G S E P S D I I I P L R - - - T A D S V F C P H Y E K V S G D Y G H P V Y I V Q E M P P Q S P A
AL2.sht    285 P R E A E P G E L G I A L R G G G A A D P P F C P H Y E K V S G D Y G H P V Y I V Q D G P P Q S P P
AL2.long   285 P R E A E P G E L G I A L R G G G A A D P P F C P H Y E K V S G D Y G H P V Y I V Q D G P P Q S P P

lerk2      341 N I Y Y - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
huHTKL     328 N I Y Y - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
AL2.sht    335 N I Y Y - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
AL2.long   335 N I Y Y T S I S V L E W P I L H T I Q L F F M R S K C S R V T T F L F P V Q V I T T S T C R M T S F
```


FIG._4B

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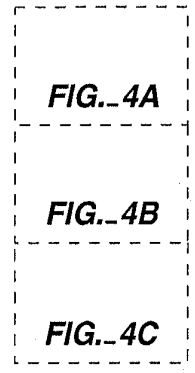
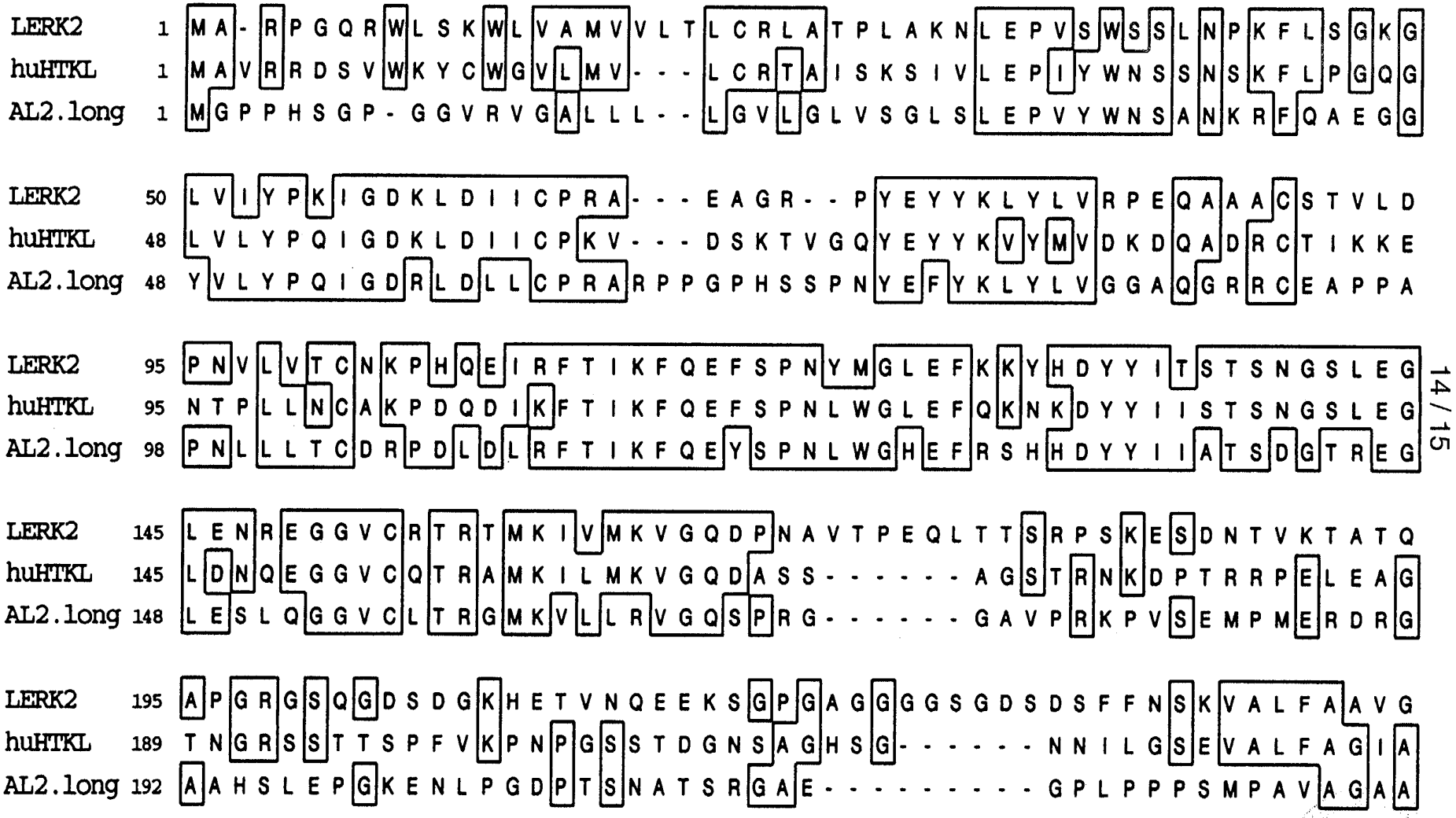
lerk2      345 - - - - - - - - - - - - - - - - - - - - - - - - - - K V - - - - - - - - - - - - - - - - - - -
huHTKL     332 - - - - - - - - - - - - - - - - - - - - - - - - - - K V - - - - - - - - - - - - - - - - - - -
AL2.sht    339 - - - - - - - - - - - - - - - - - - - - - - - - - - K V - - - - - - - - - - - - - - - - - - -
AL2.long   385 S F T T L N P S M Q A C R A Q M G E F R I R W C F W G D R I L G T A L F V L V L I L L L G R L N M H

AL2.long   435 Q T T L L R Q R A S V E A E A G Q H G P L
```

FIG._4C

FIG._4

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huHTKL 1 MAVRRDSVWKYCWGVLMV---LCRTAISKSIVLEPIYWNSSNSKFLPGQG
AL2.long 1 MGPPHSGP-GGVRVGALLL--LGVLGLVSGLSLEPVYWNSANKRFQAEGG
LERK2 50 LVIYPKIGDKLDIICPRA---EAGR--PYEYYKLYLVRPEQAAACSTVLD
huHTKL 48 LVLYPQIGDKLDIICPKV---DSKTVGQYEYYKVYMVDKDQADRCTIKKE
AL2.long 48 YVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPA
LERK2 95 PNVLVTCNKPHQEIRFTIKFQEFSPNYMGLEFKKYHDYYITSTSNGSLEG
huHTKL 95 NTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNKDYYIISTSNGSLEG
AL2.long 98 PNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREG
LERK2 145 LENREGGVCRTRTMKIVMKVGQDPNAVTPEQLTTSRPSKESDNTVKTATQ
huHTKL 145 LDNQEGGVCQTRAMKILMKVGQDASS------AGSTRNKDPTRRPELEAG
AL2.long 148 LESLQGGVCLTRGMKVLLRVGQSPRG------GAVPRKPVSEMPMERDRG
LERK2 195 APGRGSQGDSDGKHETVNQEEKSGPGAGGGGSGDSDSFFNSKVALFAAVG
huHTKL 189 TNGRSSTTSPFVKPNPGSSTDGNSAGHSG------NNILGSEVALFAGIA
AL2.long 192 AAHSLEPGKENLPGDPTSNATSRGAE---------GPLPPPSMPAVAGAA

FIG._5A

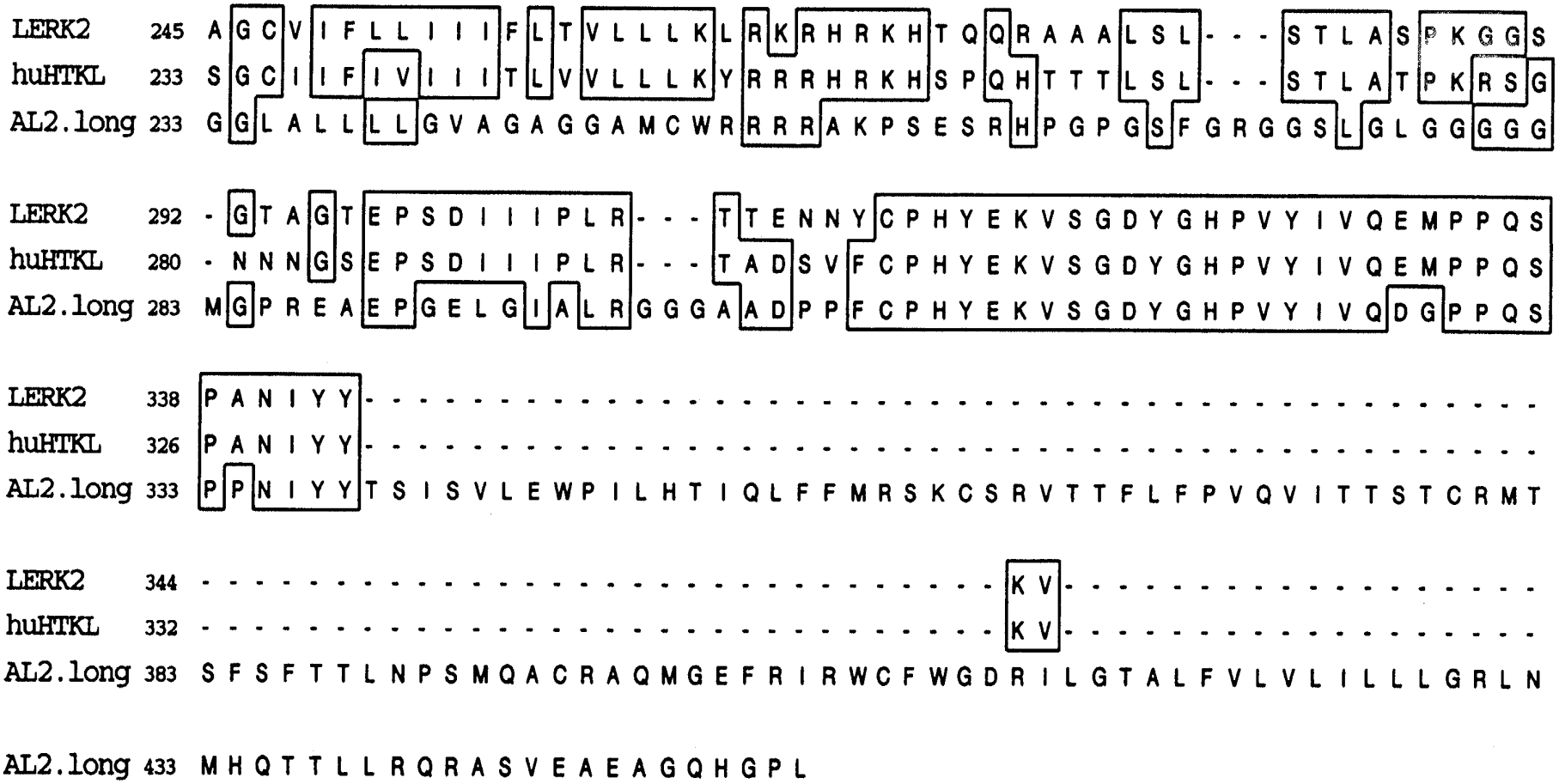

FIG._5B

FIG._5A

FIG._5